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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1: 9b ba1:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AF055578 AF228338 E10125 E10126 AF002460 AF056936

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LOCUS
DEFINITION .
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KEYWORDS
SOURCE
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TITLE
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Bacillus stearothermophilus
Bacteria, Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
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SECRETION OF CARRIER BONDED PROTEINS INTO
EXTRACELLULAR SPACE
PALCH: WO 9906567-A 11-FEB-1999;
LUBITZ WERNER (AT); RESCH STEPHANIE (DB)
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M69183 plasmodium
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VELTAVPVNGTLKLQLSAAANEDTVNVNTVRIYKVDGNIPFALNTADVSLSTDGKTIT
VDASTPPENNTEYKVVKGIKDKNGKEEKEDATTEKLABAVVTOVEGTNVTNNTSVN
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2940	gtattcactccatctcaagaattaaaagctggtacagtttactctgtaacaattgacggt	2881	QY
2880	GCAGCAGGTAATGCGGTAGCTGGTAACAGCATTAGACGGTTCTACAAATAAAT	2821	В
2880	cagoaggtaatgoggtagotggtactgtaacagcattagacggttotacaaaataaatt	2821	ν
2820	TGAATTCAATGAAACTGATTTAGCGGAAGTTAAACCTGAGAACATCGTTGTTAAAGAT	2761	Db
2820	ttgaattcaatgaaactgatttagcggaagttaaacctgagaacatcgttgttaaag	2763	Qy
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2580	TTAACTGGTCTTGACAATAACGACAAAGATGCGAAATTGCGTCTGGTAGTAGATAAGTCT	2521	趽
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2520	ACTGTATCAGTTGCTCCT ANGACAGATGCAAATGGTAAAGTAACAGCTGCTGTGGTTACA	2461	용
2520	ctgtatcagttgctcctaagacagatgcaaatggtaaagtaacagctgctgtggtta	2461	Qγ
2460	GCCAAAGTAACTGTCGAGAAATTAACAAACAACGGATGGGTAGATGCTGGTACTGGAACA	2401	ర్జ
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2340	AAAGGTGATTCTTTAAAAGACGCTGATGCAGTTACTACACTTACGAACGTTGATGCAGGT		망
2340	ytgattotttamaagacgotgatgoagttactacacttacgaacgttgatgcagg	2281	γo
2280	ATCTATACATTTACAACTGAAGGTCAAGACGTAACAGCACCAACGGTTACAAAGTATTC	2221	용
2280	totatacatttacaactgaaggtcaagacgtaacagcaccaacggttacaaaagtatt	2221	Qy
2220	AAAGGTGCAACAGCTCCTGTTAAAGATGCTGCAAATGCAAATACTTTAGCAACTAT	2161	ઠ
2220	ggtgcaacagctcctgttaaagatgctgcaaatgcaaatactttagcaactaact	2161	Qу
2160	GTGAAAGTTGCTGCTAACCAATTAGAACGTAACCAAGGGTACAAATTAGTAGTGTTCGGT	2101	당
2160	tgaaagttgctgctaaccaattagaacgtaaccaagggtacaaattagtagtgttcgg	2101	Qу
2100	GCAAGTGACATCCAGCTAGTGTGAAGCGGTTACTGGTCAAGATGGAACATACAAA	2041	당
2100	aagtgacatcattccagctagtgttgaagcggttactggtcaagatggaacatac	2041	Qy
2040	ACAATCACATACGGTCAAGTTGCTGTAGTAAAAGCGGGTGCAAACTTATCTGCTCTTACA	1981	ర్జర
2040	ant cacatacggt caagttgctg tagtaaaagcgggtgcaaacttatctgctctta	1981	VΩ
1980	TTTACTGTGAAGTTCTCAGAGAATTTAAATACATTTAATGCTACAACCGTTTCGGGTAGC	1921	닭
1980	ttactgtgaagttctcagagaatttaaatacatttaatgctacaaccgtttcgggtagc	1921	Qy
1920	GTTATTAGCGTAACGTCTAAAAATGGCGACGCTGGATTAAAAGTAACTGAAGCTCAAGAA	1861	8
1920	ttattagogtaacgtotaaaaatggoggoggotggattaaaagtaactgaagotcaagaa	1861	Qy
1860	TTAGGCACTGTTAACGAGAAAACATATGAGTTCAAAACTCAAGACTTAACTGCTCCTACA	1801	용
1860	aggcactgttaacgagaaaacatatgagttcaaaactcaagacttaactgctccta	1801	γo

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M Bacillus stearothermophilus
Bacteria; Firmicutes; Bacillus/Clostridium gr.
Bacillus/Staphylococcus group; Bacillus.

1 (bases 1 to 3687)
Lubitz, W. and Sleytr, U.
RECOMBINANT EXPRESSION OF S-LAYER PROTEINS
Patent: WO 9728263-A 07-AUG-1997;
LUBITZ WERNER (AT); SLEYTR UME (AT)
LOCATION/Qualifiers
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Kuen,B., Sleytr,U.B. and Lubitz,W.

Sequence analysis of the sbsA gene encoding the 130-kDa surface-layer protein of Bacillus stearothermophilus strain Gene 145 (1), 115-120 (1994)

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Jarosch,M., Egelseer,E.K., Mattanovich,D., Sleytr,U.B. and S-layer gene sbsC of Bacillus stearothermophilus ATCC 12980:
molecular characterization and heterologous expression in
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Bacillus stearothermophilus
Bacteria; Firmicutes; Bacillus/Clostridium
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On Apr 13, 1999 this sequence 
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Jarosch, M., Egelseer, E.
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Jarosch, M., Egels
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/product="surface layer protein
/protein_d="AAC12757.1"
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 GCGAAAGCGCAAATGAAAGAAGCATACTATACGTACAGCCACACGGTAACGGAAACGGGC
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Danhorn,T., Egelseer,E.M., Idris,R.,
Dlrect Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence update by submitter on Jul 14, 2000 this sequence version
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Submitted (24-JAN-2000)
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Danhorn,T., Egelseer,E.M., Idris,R.,
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                 DOI H., Nngakuchi Y., Tanaka Y., Fujisaki Y., "GENE CLONE MANIFESTING CHICKEN LEUCOCYTOZOON IMMUNOGENIC RECCOMBINANT VACCINE AGAINST CHICKEN LEUCOCYTOZOON"; Patent number JP 1995284392-A/1, 31-OCT-1995.

DOUBUTSUYOU SEIRUTSUGAKUTEKI SEIZAI KYOKAI, KITASATO INST:
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Doi H., Nagakuchi Y.,
"GENE CLONE MANJESTII
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                 AGAAGAAGAAAAGT AACACATGAAGAAGAAGAAAAAGTAACACATGAAGAAGAAAAA
                                gcgcgaagtacaagacgctgtgaaagcaggcaatttagacaaagctaaagctgctgttga
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/db_xref="taxon:32644"
/organism="unidentified"
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/strain="shizuoka"
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DOÍ H., Nagakuchi Y., Tanaka Y., Fujisaki Y.; GENE CLONE MANIFESTING CHICKEN LEUCOCYTOZOON IMMUNO RECCOMBINANT VAJCINE AGAINST CHICKEN LEUCOCYTOZOON*; Patent number JP 1995284992-A/2, 31-OCT-1995.

DOUBUTSUYOU SEISUTSUGAKUTEKI SEIZAI KYOKAI, KITASATO
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JP 1995284392-A/2
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                                     AGT AACACATGAAGAAGAAGAAAAAGTAATACATG---AAGAAGAAGAAAAAAGAAGAAGA
                                                                                                                                  AGAAGAAGAAAAGT AACACATGAAGAAGAAGAAAAAGTAACACATGAAGAAGAAGAAAA
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                                                                                                                                                                                                                                                                             AGAAGAAGTAACACATGAAGAAGAAGAAAAAGTAACACATGAAGAAGAAAAAGAAGT 2483
                                                                                                                                                                                                                                                                                                                                           caactatgcbacaaaattagacgaaatgcgccaagagctagaggctgctgttcaagcaaa 443
                                                                                                                                                                                                                                                                                                                                                                            cgttttcaaagcaaaccctaaatctggcgaagctcgtgtagcaacttacatcgatgctta 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATACATGAAGAAGAAAAAGAAGTAACACATGAAGAAAAGAAAAGAAGAAGAGCATGA
                                                                                                         tcaaatcaatcaatacttaccaaaagtaacagatgctttcaaaaactgaactaacagaagt 743
                                                                                                                                                                                                                                                                                                                                                                                                                          AACACATGAAGAAGAAGAAAAAAGTAATACATGAAGAAGAAAAAAGAAGTAATACA
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/note-"immunogenicity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=Fip9
Genes with similarity to proteins in the databases are described product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://ccR-081.mit.edu/GENSCAN.html), NetGene2 '(S.M. Hebsgaard, et al., CBS, Technical University of penmark, http://www.cbs.dtu.dk/services/NetGene2/) and spijcobredictor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (06-JUN-2000) to the DDBJ/EMBL/GenBank databases Yasukazu Nakamura, Kazusa DNA Research Institute, Department Plant Gene Research, 1532-3, Yana, Kisarazu, Chiba 292-0812, (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                splicePredictor (Volker Brendel, Stanford University, http://grenlinl.zool.iastate.edu/cgi-bin/sp.cgi)
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, http://genome.wustl.edu/eddy/tRNAscan-SE/)
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Magnoliophyta; eudicotyledons;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Address for correspondence: kaos@kazusa.or.jp
Ror the latest information on annotation of this clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura,
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                                                                                                                                                                                                                                                                                          sequence may not be the entire insert of this clone.
                                                                                                                                                                                                                                      r because we remove overlaps between neighboring clone is T8N9 and the 3' clone is T7B9.
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complement(join(4747.
                           /clone_lib="IGF BAC"
                                                                            /db_xref-"taxon:3702"
/chromosome-"3"
                                                                                                                                                                                                           Location/Qualifiers
                                                 /clone-"F1D9"
                                                                                                                                   /strain-"Columbia"
                                                                                                                                                       organism="Arabidopsis
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.5195,5297.
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dicots; Rosidae;
.5754,5827
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                                                                                                                                                                                                                                                                  submissions
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complement(25073, .29379)
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10in(21817...22014)
/note="contains similarity to Aff-dependent CLPB protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence-not_experimental
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/note-"contains similarity to ATP
gene_id:FID9.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /pseudo
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/fote="contains similarity to
polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"contains similarity to unknown gb|AAC97228.1
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8311 .8737,9083 .9347))
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45043. .45198)
                                                                                                                                                                                                                                                                                                                                                                      /pseudo
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/poin(30097 . 30190,30265 . 30551,30614 . .31510,31758 . .32036)
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join(11589 11736,11836 12019,12305 12497,12774 12896,
                                                                                                                           /note="gb|AAD25852.1
gene_id:F1D9.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene_id:F1D9.5"
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/evidence=not_experimental
join(46889. .47780,47984. .48332,48695. .48783)
                                                                                               strong similarity to unknown
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/evidence-not_experimental
/protein_id-"BAB01984 1"
/brotein_id-"BAB01984 1"
/db_xref="GI:9294133"
/transiation-"MLSKVKIPLPDLMSSVLALDESVIDVDQVDNLIKECPTKEBAEL
LKGFIGNKEFIGRCEGFFLELLKVPKVETKLKVPSFKIQPHSQVRGSTKLKRIMQTIL
SLGNALNGTARGSAIGFHLDSLIKLIPDTRSNSKMTLMYLCRGVLABELPGLLNFP
KDMIQLKYLAEEMQATSKGLEKVVQEFTASETDCQISKHFHMNLKEFLSVAEGEVRSL
ASIL'STVGGSADALALYEGEDPARVPFEQVVSTLONFVRIFVRSHEENCKQVEFEKKR
AQXEAENEKLKKGYLNEN"
compiement(66524...66974)
.note-"gbiAAD23008.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="maize transposon MuDR protein-like" complement(join(63866. 64008,64160. 64226,64346. .64414,6450. 64504. .64520,64743. .64790,64956. .65053,65183. .65264,65486. .65566,65677. .65718,65854. .65952,66106. .66144))
'/note="contains similarity to human diaphanous legene_diFID9.13"
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33433 .53558,53717. .53803,53908. .54010,54110. .54210,
54472. .54531,54627. .54728,54795. .55047,55142. .55226,
55334. .56657,57220. .57389,57601. .58187)
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complement(join(58782. .58995,59066. .59150,59231. .59498,
60276. .61922,61970. .62259,62305. .62482))
/note="gene_id:FID9.12"
                                                                         strong similarity
                                                                                                        gene_id:F1D9.18
                                                                                                                             /evidence=not_experimental product="copia-type reverse transcriptase-like protein" complement(join(81294 ..81521,81620 ..82285)) /note="gb|AAD23008.1"
                                                                                                                                                                                                                                                                                       /note="emb|CAB75469.1 gene_id:F1D9.17"
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/product="retroelement pol
compiement(75178...76058)
/note="gb|AAD23008.1
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71526. .72709,72898. 73300,73370. .73533,73687. .74594)}
/note="gene_id:F1D9.15"
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                                                            malaria parasite P. fa
Plasmodium falciparum
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1 (bases 1 to 5420)
                                                                                                                                                                AF056936 5420 bp DNA INV 13-APR-1998 Plasmodlum falciparum mature parasite-infected erythrocyte surface
         binds human erythrocyte protein 4.1 Mol. Biochem. Parasitol. 50 (2), 335-347 (1992)
                                   Repeat structures in a Plasmodium falciparum protein
                                                 Coppel, R.L.
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88953. .89075,89158. .89715))
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2 (bases 1 to 5420)
Kun, J.F. J., Waller, K.L. and Coppel, R.L.
Plasmodium falciparum: Structural and functional domains of the
mature-parasite-infected erythrocyte surface antigen (MESA/PfEMP2)
Onpublished
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FEQMIGENELCHKHLET EDEERTLYVKDDAKKHKLLGEGD
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KEDVKEKNDEQKDKYLGEGD KEDVKEKDEQKD KYLGEGDE EDVKEKNDEKTIG
GIKENDEQKDKYLGEGIKENDTEGNDKYKGPEILTEEVKE
EIKHVEEGIKENDESKDKVLGQELTIEEVKERDE KRONTEGNDKYKGPEILTEEVKE
EIKHVEEGIKENDTESKDKVLGQELTIEEVKERDE KRONTEGRENKDKVIGPEILTEEVKE
LIEGDEKGNEENILEIKDIVLGQEVILEEVKDIKNDEGGENKDKYTGGEVE
VKKEVKEKGNKENILEIKDIVLGQEVILEEVKEVEKGIKENDTESKDKVLGGE
LIVEBYKEELEKQVEBGIKENDTESKDKVIGGEVIKODVNEBGGENKDEVTKQEKVE
VKKEVKEEVKEKEEVKEKENVESKONVIGGEVIKODVNEKDTANKDKELEGGEKEEVKEKDTESKDK
EKEEVKEKEVKEKEVKEKENDVIGGEILEELKEVKEKEVKEKEEVKEKDTESKDK
EKEEVKEKEVKEKEVEKEKENTOLESKOLVIGGEILIEELKEVKEKENTKENKNENKONVIVQ
EINNELLAKDTANKDKVIEGEKEEVKEKEEVKEKEDVKEKEVKEKEVKEKENTOLESK
KDKELEGEKEKEEVKEVENEKEDTENDKVIGGEILIEELKEVKKEKEVKENKNENKDNV
VIVQELMHEDVNEKDTANKDKVIEGEKEESVKEKEDVKEKEDVKEKENTERDK
DKELEGEKEKEEVKEKENTENDKOLTGGEILIEELKEVKKEKDTUKKRVIGGEVILEEVKERD
VKKRVKERNNKNENKDVIVQELMHEDVNEKDTANKDKVIEGEEVKEKETKERVKERKDKVEKDTUKROTTGOEVILEEVKERD
VKKRVKERNNKNENKDVIVQELMHEDVNEKDTANKDKVIEGEEVEETKERETKERTOLETEGEETKE
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//BLXTef="GI:3044185"
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//LTAINS1ATION="MEUTCRNLCYDKKNNMMENBGNKVKKVYNNSSLKKYMKFCLCTI
ICVFLLDIYINCESPTYSYSSIMNNUDRYVRILSETEPPMSLEEIMRIFDEDHLYSIK
NYIECLRNAPYIDDPLNGSVYTDNKNNCLOHIKLLEMOESERRKOGEBENAKOLEEI
RKKEKTYLMKELEMDESDVEKAPRELOFIKLDRITRPKHVNVHGESKEIDESKEITESKET
ESKETTGESKETGETGESKETGETGESKETGETGESKETGETGETGETGETGETGETGETGETGE
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0; Mismatches 530;
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                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 179553)
Waterston, R. H.
 2 (bases 1 to 179553)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                             ACO24253 179553 bp DNA RTG HOMO Saplens chromosome 6 clone RP11-758C19, SEQUENCE, 12 unordered pieces. ACO24253
                                               The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                               Homo sapiens
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                                                                                                               Hominidae;
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On Jun 16, 2000 this sequence version replaced g1:7235339.
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Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 175235 bases at least 040
Consensus quality: 175235 bases at least 030
Consensus quality: 177171 bases at least 030
Consensus quality: 177171 bases at least 020
Insert size: 198000; agarose-fp
Insert size: 198000; agarose-fp
Quality coverage: 4.99 in 020 bases; sum-of-contigs
Quality coverage: 4.99 in 020 bases; sum-of-contigs
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Sequencing vector: plasmid; 0%
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Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                2884 32983: gap of unknown length
2984 43009: contig of 10026 bp in length
3010 43109: gap of unknown length
3110 52414: contig of 9305 bp in length
2415 52514: gap of unknown length
2515 78544: contig of 26030 bp in length
8515 78644: gap of unknown length
8515 78644: gap of unknown length
8615 107099: contig of 2845 bp in length
7100 107199: gap of unknown length
7200 133717: contig of 26518 bp in length
3718 133817: gap of unknown length
3818 179553: contig of 45736 bp in length
179553: contig of 45736 bp in length
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/note-"assembly_name:Contig8
clone_end:T7
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/note="assembly_name:Contlg9"
16535. .24088
                                                                    vector_side:right"
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32984. .43009
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107200. .133717
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43110. .52414
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RESULT 11 PFMAL4P1_1

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PFMAL4P1_1
PFMAL4P1_2
PFMAL4P1_3
PFMAL4P1_3
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                                                                                                                                                                                             gtgtaagtgcgattaacactcaaaacaaagctgttgaattaacagcagtaccagtgaacg
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                                                                                                                                                                                                                                                              ATGATAATGACGATGTTAATGAAATTAATAGTGAGAAAAATAAAAAATCAGCTCGTAAAT
                                                                                                                                                                                                                                                                                                                             AAGAAAATGATGATAACGAAGAAAATGATGATAACGAAAAATGATGATGAAGAAAAATG
                                                                                                                                                                                                                                                                                                                                                   cagaagtagcgaaaaaagcattagatgcagatgaagctgcgcttactccaaaaagttgaaa
                                                                                                                                                                                                                                                                                                                                                                                           ATGATGAAG AAAATGATGATGAAGAAAAATGATGATAACGAAGAAAATGATGATAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgaaagcgcgaagtacaagacgctgtgaaagcaggcaatttagacaaagctaaagctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGAMAATGATGATGACGAAGAAAATGATGATGATGAAGAAAATGATGATGACGTAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgastaaagcaggtggcgcgaaaaaaggacgcttacttagctgatttscaaaaaggaatstg
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$76368.1
   Saimiriine herpesvirus
                                                              [herpesvirus 3720 nt].
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ilarity 43.2%;
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.ECRF3=G protein-coupled rec.
1 HVS, host-squirrel monkey,
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from b
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Pred. No. 0.1;
D; Mismatches 403;
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 host-squirrel monkey.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saimiriine herpesvirus 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptors and cyclins
Nature 355 (6358), 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpesvirus saimiri encodes homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholas, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gammaherpesvirinae; Rhadinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r [NCBI gibbsq 76368] from sequence comes from figlb.
           /protein_id-"AAB21117.1"
/protein_id-"AAB21117.1"
/db_xref-"GI:243354"
/tramsia_tion-"MEVLYREDESEDESNYSYNYSGDIYYGDVAPCVVNFLISESALAF
/tramsia_tion-"MEVLYREDESEDESNYSYNYSGDIYYGDVAPCVVNFLISESALAF
-TYVLMFLCNALGOSLYURTEHKYRAQAQSEDYLMMGPCLNSLPLAGYLLMRLLRMFEI
ENNTBLCKLEAFFLNLSIYWSDFILVFISVLRCLLIFCATRLWVKTILIGQVFLCCSF
-VLACFGALPHVMVTSYYEPSSCIEEDGYLTEQLRTKLMTFHTMYSFAGDLFITYICYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MADSPNRLNRAKIDSTTMKDPRVLNNLKLRELLLPKFTSLWEIQ
| PEYTVONRTILLTWMHLLCESFELDKSVFPLSVSILDRYLCKKGGTKKTLQKIGAAGV
| LIGSKKRTYREPMTVSKLVTYLSCUCFTWLLELIKPGEXDILEALKWDTEAVLATDFLILFLC
| NALKIPEDLWPQLYEAASTTICKALIQPNIALLSPGLICAGGLLTTIETDNTNCRPWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MDLKTTVLHITDSFTDEEMYCLLFLINGCIPRSCNAVNISDLII
.ETLSKSTQWD1CLMQCL"
complement(95. .977)
/gene-"ECLP2"
   MSCYKLFKTKLSKRAEVVTIITMTTLLFIVFCIPYY IMESIDTLLRVGVIEETCAKRS
                                                                                                                           /note="G protein-coupled receptor homolog;
comes from fig1b"
                                                                                                                                                                                                                                                            SLSFPGAVSSGIQTFPKGPHATGPWYYFITYYCRTFQTAKEYIKAQKKYEKKYPRSAK
                                                                                                                                                                                                                                                                             EBAEBAEBAEBABBEABEBEBEAGPSTPRLPHYKVVGQKPSTQPGGVPKLCLKMQPQH
RSRLPKGKQSHDKVPKXYQARNKFFSQAAPSVLDLSPKSWCWVVDFWGPTDALYRLSR
                                                                                                                                                                                                                                                                                                                         complement(1004. 2227)
/gene="ORF 5' of ECRF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ORF 5' of ECRF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYLEDLSSILNESTWIVRTVKDQVSEAFSLYDLEIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="cyclin homolog"
complement(184. .948)
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                                                                                                                                                                                                                                          LKASLGKFSKSLPIE"
                                                                                                                                                                                                                                                                                                            complement(1.
                                                                                                                                                                                                             /gene-"ECRE3"
                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAB21116.1"
/db_xref="GI:243353"
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="This sequence comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAB21115_1"
/db_xref="GI:243352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene-"ECLF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAB21118.1"
/db_xref="GI:243355"
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complement(1. .194)
                                                                                                                                                               /gene="ECRF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="cyclin homolog; This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=
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                                                                                                                                                                              ="G protein-coupled .3691
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Best Local S
Matches 2I1
                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I924
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                                                                                                                  SgS
                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1684 GAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1864 GAAGCTGAAGAAGCAGAAGCTGAAGAAGAAGAAGCTGAAGAAGAAGCTGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1624 GAAGAAGCTGAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IO aaaaaagctgtgaaactagcaacagcaagtgctattgcagcaagtgcatttgtcgctgca 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 2I1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGCTGAAGAAGCTGAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGAAAAAGAAGCTGAAGAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aatccaaacgcttctgaagcggctacagatgtagcaacagtagtaagccaagcaaaagca 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gctgttcaagcaaaagatttagaaaaagcagaacaa 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tacatcgatgcttacaactatgcaacaaaattagacgaaatgcgccaagagctagaggct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaatatgaaacttacgttttcaaagcaaaccctaaatctggggaagctcgtgtagcaact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGCTGANGAAGNNGCTGAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGAAGAAGCT 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aacattaacgatgtatatgctgaatacaacaacgaaaaacgataccgtgatgcggta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cagttcaaaaaagcatactatacttacagccatacagtaacggaaactggtgaattccca 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M86409.1 GI:330976
DNA-binding protein; capsid protein; dUTPase; ribonucleotide
reductase large subunit; ribonucleotide reductase small subunit;
reductase large subunit; annihase: transactivator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSV3PRGEN 43658 bp
Herpesvirus saimiri 1
M86409
                                                                                                                                                                                                                                                                                                                                         Nicholas,J., Cameron,K.R., Coleman,H., Newman,C. and Honess,R.W. Analysis of nucleotide sequence of the rightmost 43 kbp of Herpesvirus sainiri (NVS) L-DNA: General conservation of genetic organization between NVS and Epstien-B arr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage;
Gammaherpesvirinae; Rhadinovirus.
1 (bases 1 to 43658)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpesvirus saimiri (strain 11)
Saimiriine herpesvirus 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transpressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tegument protein; thymidylate synthase; transactivator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I.7%;
milarity 45.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  921
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3 731 c 675 g 1393 t
                                                                                                            complement(I 409)
                                                                                                                                          /organism="Saimiriine herpesvirus
/strain="11"
/db_xref="taxon:10381"
                                                                                                                                                                                                                               1. .43658
                                                                                                                                                                                                                                                         Location/Qualifiers
/protein_id="AAA46126.1"
                          /codon_start=1
                                                       /note="first methionine
                                                                                        /partia
                                                                                                                                                                                                                                                                                                                 296-310 (1992)
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); Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       most three prime
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                                                          in
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                                                          the
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                                                          EDLF5 ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 '/note="EDRF1 ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILLSHCREKCTGLWRNYGTEKSYLMGLGKEITLCYQALNESGITYSTTLAAFIKLSFP
TISIPHLFERPEQSCKGNQDREPDICTOGSYLKEPHQGYTGDTPFIDDPLMEELSENG
FKKFSTANISTLLQNFKEILEMDPFDFRIGGPLNKEETATPLKDSSFSNPTFIVTGA.
ANTLLPAASYTPALESLFSPTHEFPCHSDESLASTSHYDLDNNISLPTLYKTHEPLERE.
RQSRNIDPNTPERRPRGFRKGSKTKKRPTCSPALFQSSDIPTDSLHYKCPEMLPTVPQN
EFCDSSNIQPCTSSSYLENDNLYPINEAETDDNILATILQDLYDLPAPPYLCSHENCT
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LRRFFLRNDLGFLSAVVILKQYVENLFTTKQKLNLIECTQGLKFLIRSLYEKIKDQCD
VKSSIREIFYDCKARLLLLLLEEGCGCGACCATSA"
                          nucleotidohydrolase"
/EC_number="3.6.1.23"
/note="first methionine codon
                                                                                                                                                                    /protein_id="AAA45130.1"
/db_xref="GI:330982"
/transiation="mTwklficflspgviflryssltekshttsytilhnnnfysnsc
sadyvypsiktessymailnviiffcaslfylrhlcivkfisnltk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="EDLF3 ORF"
Complement (165)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="transpressor"
/product="transpressor"
/protein_id="AAA6128.1"
/protein_id="AAA6128.1"
/db_xref=="(di:330980"
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/translation="MKAQALLCSlvLLAQSTDVDDEGSGEVFIOKVSSSVSITASLA
/translation="MKAQALLCSlvLLAQSTDVD"
/tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEIDNNVDIEDLGLSFPMSLQDFLNDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="noripiwivrsthclillfoddvqvrkscleptiflsperkrei
HQLLvafnqslytptqdbekilsdiqraciqiaedikhlnptggiyldulvtlwtll
RNYKTKQRSQpvnstyvsryahhyvxximqrivttdrlflyptsgiyldvplanai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="transactivator"
/protein_id="AAA46124.I"
/db_xref="GI:330979"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <1491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSRPYOPORYSLISELHKNFHYVDVSVIOSEFKNVILKTVVPKL
SQPAPHLEKGDFLLKIQQLLMHREEDQOILMKVKSNIIYFLNEIMSAEYGKVQEOVK
NILCEVKLDKTDSELSTYLAOBIPKLTYLKTPHFKVCETIPMGRWCLHNILGIEQY
YKDFSNIVLHDPETSLGSVQAYSRLSKILFWCDSFNNKIYPCNAFNSSINQVYLMSTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(604. .609)
                                                                                                                                                                                                                                                                                                                                                                                                      complement(4549.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="5' end of coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FHFYSVAHCNDCISESISFTEALLKQEVSAFYEWCLEEEYEEDRMAKFMKFSADQITI
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                                                                                                   /standard_name="deoxyuridine
                                                                                                                                                                                                                                                                                                                                                 complement(4550
                                                                                                                                                                                                                                                                                                                                                                                                                                 NLSRRPASKPRTK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAA46129.1"
/db_xref="GI:330981"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLKPFKPKTQPIVNMQRTWIYPLTGIVSIVVLLIINSCIHCYIRRFDEHFE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"first methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                            /note="EDLF2 ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              aqkdaiinstynkltkkaeekirerylkdylplysknqcmeaiahikyridysidety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="EDRF2 ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:330978"
                                                                                                                                                                                                                                                                                          'codon_start=
                                                                                                                                                                                                                                                                                                                    /note="first methionine codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation-"MASRRSCADVEELEKELQKLKIENKALKKKLVQHTSPEDELLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methionine
                                                                                                                                                                                                                                                                                                                                                 .4822)
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                                                                                                                                                                                                                                                                                                                    in the EDLF2 ORF"
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                                the EDRF3 ORF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDLF3
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polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCLNKDIFIKYSHLINSDNIHFYPETEYLAQSLDENFRKDMLTYYNKSTYLKIYITHK
CIHLEDLIGYAPQDCTSEYYMAGQSKUHNLLNYINTHHHHINISEDLNGLLDLAAID
STENDDLIGYAPQDCTSEYYMAGQSKUHNLLNYINTHHHHINISEDLNGLLDLAAID
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LKDTEITSNIEYKETETSALTLADQLKISHTYFYIVONDILKLAVIDLDLHIHTSEBHYI
LKDTEITSNIEYKETETSALTLADQLKISHTYFYIVONDILKLAWIDLUBETDGFPDVGIYK
CGFRI TYPLAGVVLLCSNDYISFVNILNRTIKITKIDKKLLAWIDLIMETDGFPDVGIYK
KGCYRI PHTYKNISGRLERLLKLEYCHPHYDNKLQYYNDISPDINNLIYHSHIPEKY
KQLKAVUDIADINENFILQKAQAQLPQTNHNAVERIESASHMSITDWYAEETAMPRIFE
LIKLYLSEEKYSQFYHYSFAASTGNIIKIISLSGNFSCLNFKHRLKTQSVRIFILSLHL
                                                                                                                                                                                                                                                                          LPVPSLPCQEAEKTNDKYVLAMAQRAMHDVPISSKQLTANLLPVKEKPLLSIVRYTPN
YYMYSMRKETIASANLCTVAAFLDESLCWGQQYLKNDFIFSENGKDIILDTSSALLS
QLVHKIKMLPFCHCLMQTTPQDHIVKQYCYLLASNNRILDAVRYLQTSVIKSFTVLLL
AYAVCLPAAIICTKNETYQLYSHCMRILKEYRPGDVMNILHESLTQHLNKCPSSTCAYT
TRAIVCTKANTTGLFFLFTQ"
                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"transactivator"
/product-"transactivator"
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/db_xref-"GI:330986"
/translation-"YLGHISDDDFDSSDSSSDEEESDTSPQIMKSDVTMASPPSTPEP
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SPDVSASTSNLKRERQRSPITWEHQSPLSKVTRSPSPMRFGKRPRISSNSTSRSCKTS
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WADRVEEAAAQRRPSRPFRKFYSHPRNGPLRNGPPRAPPLKKLFDISILPKSGEPKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="EDRF4 ORF"
complement(9074. 9079)
/note="EELF5 ORF"
<9082. 10320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="required for DNA replication"
/protein_id="AAAA6133.1"
/protein_id="AAAA6133.1"
/db_xref="GI"330985"
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/translation="MURATEAMPKEKVLFATDGDSAEIITDILTGTDTNAFIYSYLHN
CYIYPTEVKIVLILCLPAKKPGGGDKCLEVFQLHIDTELAIPFLFYTKPLKANDLHKY
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                     MITTIFGSFEVPFLLTALFYFFBOHNCTINTIFHLSSLFEKKLGTSLIAITTFEELGGV
CSTSDYLKTAPAFINYCHIKLARDSLESQAIDTSIDTLRGQLMLSNQDLVHYIYLSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="M.QWLHSCWPFGKYRRQKYVPLDTSSSCPDRWKIEIEIAQPPGV
FVGDILQNSDSDASLRQAYLLAVQLNNITDYLKRFDEASYPESCKSVVQTQITKLKSV
RNIIWTMLSKAVGGVTIDDAALKTLLDKRAGESIALIEMEKLATATVDDSKAWAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="EDLF1 ORF"
complement(5797 ..6399)
/note="first methionine"
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LGAVLFLLAVEFASVVSVVQRLDIFVGMQNYLFLLFVSMLCCCMFSLPSNAICVVLET
                                                                                                                                                                                                                             complement(10679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPDNCVTLTLMSQCFASKCNSNKCIAHMSVRVPITDK"
                                                                                                                         /protein_id="AAA46134.1"
/db_xref="GI:330987"
                                                                                                                                                                                                   /note="first methionine
                                                                                                                                                                                                                                                     /note="EJRF1 ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="5' end of coding region
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="first methionine codon in the EDRF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INNIILSAEHEKQILVNSEVPLIECETLAAEKTTTPAVSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA46132.1"
/db_xref="GI:330984"
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/protein_id-"AAA46131.1"
/db_xref-"GI:330983"
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ORGANISM
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SgS

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no RNA stage; Herpesviridae;

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Query Match
Best Local Similarity
Matches 211; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aatccaaacgcttctgaagcggctacagatgtagcaacagtagtaagccaagcaaaagca 129
                                                                                                                                                                                                                                                                                                                                                                       GAAGAAGCTGAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCT 37254
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gaatatgaaacttacgttttcaaagcaaaccctanatctggcgaagctcgtgtagcaact 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGCTGAAGAAGCTGAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGAAGCT 37384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGCTGAAGAAGCTGAAGAAGAAGCTGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGAAGAA 37444
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                                                                                                                  Herpesvirus saimiri
x64346
complete coding region.
Saimiriine herpesvirus:
Saimiriine herpesvirus:
Viruses; dsDNA viruses,
                                                                                          X64346.1
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complement(11774. .11779)
/note**EELF2 ORF*
complement(11774. .11779)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="EELF3 ORF" (complement(12966. .13883)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSRVVLSPKTAAMLOKWLREHKAHKTYSVMYNSTLAYLILTYEDSTKTYDLMIYDDMS
LCNNPSKDWGYVONDVOTKVNITALSAALGLCKIPGYFYPCIKFYESEYLEVCGTPVK
LGSWYDTSLQYTLFCTPNLAEDTOAAVSDYFPISPSACLTADPADTOEEPTLSSNCOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="madiqtihesygvgfkpcylgehtkiynhikakvkdgiiqiegl
TSSPSLRIWSSIGEGILSFKINNVVSEVFNCHMMPENVSVSFRNISPGGNTFLYTREL
FGCNVXTATLMFSNRSGKPFEFIKAKLEYCDKVSTTRHTSTIPAGILPFVENVNSTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="DNA-binding protein"
/protein_id="AAA46135.1"
/db_xref="GI:330988"
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                                                                                          GI:60320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name="ribonuclectide reductase beta subunit"
/EC_number="1.17.4.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function-"required for DNA replication"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primary structure of the herpesvirus saimiri genome J. Virol. 66 (8), 5047-5058 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 112930)
Albrecht, J.C., Nicholas, J., Biller, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Honess, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Albrecht,J
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KNSRLAISMNIDYWNPWSTNMLYDGLHAIERGLIYSFGSFTPTPSLTSVENMACHWY
VPMYSACCICHYWGLDLOTHELSLTGGLPKKMLCAHLKLKCSSNPHIOGFFRLYPKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"ORF Q3 similarity to ORF 75 and EBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3969. .4532)
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/gene-"STP-A11)"
                                                                                                                                                                                                                                                                                                                                                                 VIPQDKRLEMDVLDAESAVSAPLSDPLWTMSNGLFNLLGYSSQYSVFKRGAAPKVFVE
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/gene="STP-A11)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SWISS-PROT:P18347"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10381"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Saimirline herpesvirus"
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FKERLYFGNLVFIIAQGLKVQINGREAVKIPLYDEDLFSKSHEHLPRFYIPSVSKYLE
DSVFTSIAQALRIRDYESVIRASEKOSIODDYKLAKIVNSKDESLASVKCCDASLEGYV
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12584. . . 15970
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SRKFESRWSNIYIPESTKAIAFQSLKNSLIPCWTQGTHLKFYHPKPMLEKMEESGMVS
SMFYGRSLSSGPAQNYPLTPNGENAIAGVCSADGRHLALLHDPSLCNNLWQWYYVPLE
NPPLKYSPWITMELDLHKWGITVQGASPPPSRTSDPLRSFVF*
<u>APKFSGGTYTLYHLALASSFSPHLLARNCYYMQFCQHQKSTTNANYSVPQYVGTAAAS</u>
                                                     IDC I AAELAMSYGLSELEAPQDPCAVLDYTSWP I FET AET EEDR I KA I QDWAAMSVH
VYTHLEST NSYLYLTK I NKOTOSNK SEONYY NTY FWOHGLAY AADATORENGEP AF SG
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11967. .>
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11774. .11966
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YVEVPKSATSMQYLHINVKCYKGFMLYGETPNTCNHGVWSPAIPECMKISSPKGDMPG
INSNEDNSTPSGRICNGNCTTSMPTQTYTIITARYTSHIYFPTGKTYKLPRGVLVIIL
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10912. .11994
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/gene-"sccpн"
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gaatatgaaacttacgttttcaaagcaaaccctaaaatctggcgaagctcgtgtagcaact
                                                                                                               GAAGCTGAAGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGCTGAAGAAGAAGCT 106691
                                                                                                                                                                                                                                                     GRAGCTGRAGRAGCTGRAGRAGRAGRAGCTGRAGRAGCTGRAGRAGCTGRAGRAGRAGRA 106751
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                                                                                                                                                                              cagttcaaaaaagcatactatacttacagccatacagtaacggaaactggtgaattccca
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VDLKFVDGLTGAITRYLSQPKVFADDGWAGTYETRTYWNCEIVDMEARSADBYTYFV
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YSVSWEAVNKSASVCSNVFWKSFQRAIQTEHDLTYHFIANEITAGFSTVKEPLANFTS
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NLIYWSGAHKKCANVENTSEMAKLLSTEKKKONYKYICKNSPHEFDKYKPYETESI
FCGGTESSVDFUVKSIK KOCSIAFMKRANYOOLIKKONELFVELNK LIGGEDTYVSHAS
SAVPLSDKATIVNPDQVLHDAHARKDAYLQKVTKDGLKSLYTCLETOGAVLSNTLSMR
VMGGAVYDEIVKLKNHFLFDQFISLOMIHCETDSVTGFENSKYIKNLIYSGKLSSEH
LSSLTLOFYKLLTGFLGGVVSFFPLENITALANGLDAJAGALHHKKLLTENATHVSISEH
KDMVSQTYNKFYTITSTDLNSIQKEAMFFIRELVLSVSLYNEVLEKNLLVFSALNFEK
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IYLQIMPLLHAQNIESTSLSVKMCIUDLEIFSKRLSSVFYCLIRSCDALRGIMHYLDEIFSKRLSSVFYCLIRSCDALRGIMHYLDEIFSKRLSSVFYCLIRSCDALRGIMYFERHIRSLSAF
CSRHKSIVFOFYNNCCVSVKMCIUDLEIFSKRLSSVFYCLIRSCDALRGIMHYLDEIFI
HLRGVSPIPLPDTYLSNIFCIYCLNEHMMLPNQGESLPSLMMCVNCKHVCKQLNFEFI
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ITEDDLQFYLGEYYINSDEIWSRFQIITDSGAPWSVENVTKVLGCNKQEECKFEFVGV
EEQLSCYPPQIEEFAPQATLSTLAASRKKKITSILSDIDL"
15977. 18016
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LPTLQTISATEY PHVLLDQSTMSVDHYLSSIKDKHALTVQTTLKEDIATVGKQRPIVT
VPLVVNKYTGINGNTQITQCGNLGYYMGRGVDRNLTBSTGFRRONSSYMRRHYFM
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I IQDICLPIAMTYEQDNPSIGMMPSENLKYHYQTIMTIKYKSCLDRGVLTGSEHKIVH
TDMFCDFLNIDSALSGQIVPMKMQVRLAKALLTYPKTIKIKNRTVFSNSKMTETTQSE
FIKSATKKDSYIVTGPYMKFLNSLHKVMFPNAKISALYLMHTESQKKQLPVLPGISRE
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FREKEDEAVQNAESEKYTYWQL1QNVVEKLSTMGVTEGTVGSELITDIQSFLKTFRDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gardner, M.J.
Direct Submission
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Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-NOV-1998) The Institute for Genomic Research, Medical Center Drive, Rockville, MD 20814, USA
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1 (bases 1 to 12029)
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IADIKIKKEERETKDEKEKNIQQLVKDVQLIKYGEETKDDEKEDKEGTDDEEDTDDEE
DTDDEEDTDDEEDTSDBETTGDOENKEETEVDEKKTEKREEELEEDKEESEKDKEESE
KDKEESEKDKEESEKDKEKTEEDEKTETSTEVTKKETDVDEKKEKGEIGEGTDDE
EDKEKKEEDDEETKYEEKDEKGTPYEEDTDDSDKOETKYBEKKTEKDEETEEDE
EKETEVEKKKTEKDEEGTDIEDTDDSDKDVETEVEETDAEDKEENEEGTDDEEDKVE LYYESQINKNFISIPKDKIPTAIYRISNLVNDLIFLLPQSNANKAL"

BASE COUNT ORIGIN 5634 a ETDLDDQEEDGEEDKEDDKEKDKEDDKEDDKEKDKEDDKEKYKEDDKEKDKEDDKEKDKEDDKEKDKEDDKEKDKEDDKEKDKEDDKEKDKEDDKEKDKEDDKEKDKEDDKEKDKEKDKEDDKEKDKEDDKEKDKEKDKEDDKEKHDKEKHDKEKHDKEKHDKEKHDKEKHDKEKHDKEKHDKEKHDKEKHDKEKHDKEKHTIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHYDLHHIIKQQQHHIIKQQQHYDKEDQPXHYNYDEXQIEHYYNKEDQPXHYNSPEKQIEHYYNKEDQPXHYNSPEKQIEHYNSPEKQIEHYYNSPEKQIEHYNSPEKQIEHYYNSPEKQIEHYYNSPEKQIEHYYNSPEKQIEHYYNSPEKQIEHYYNSPEKQIEHYYNSPEKQIEHYYNSPEKYNSPEKYNSPEKA EFNSTNNYLMKI I NNDKLKHNSLNDNEA ILKEIT KTQNELFSLKLPLEI KYSMALRIS ERLRAFYFDKDLTAYY I KKLKDIFKLETEAAKNYYYYYKCQKTFSDKKRLVNNLDSIK 1009 ი 1093 Q 4293 t

Query Match
Best Local Similarity 43.7
Matches 336; Conservative 1.7%; 0 Score 62.6; DB 32; Pred. No. 0.3; 0; Mismatches 424; Indels Length 12029; 9 Gaps

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밁 Š 문 Ş 7917 7857 GATGATGAAGAAGATACAGATGAAGAAGAAGATACAAGTGAAGAAAACTACAGGTGAT 7916 64 4 gataggaaaaaagctgtgaaactagcaacagcaagtgctattgcagcaagtgcaatttgtc 63 gctgcaaatccaaacgcttctgaagcggctacagatgtagcaacagtagtaagccaagca 123

Ş Ş Š 7977 184 124 aaagcacagttcaaaaaagcatactatacttacagccatacagtaacggaaactggtgaa 183 TTAG AAG AAGACAAAGAAATCAGAAAAAAGACAAAGAATCAGAAAAAGATAAAGAA ttcccaaacattaacgatgtatatgctgaatacaacaaagcgaaaaacgataccgtgat 243 8036

В Ş 밁 8097 8037 244 GAATCAGAAAAAGATAAAGAAGAATCAGAAAAAAGACAAAGAAAAAACTGAAGAAGATGAA 8096 GAAAAAACTGAAGACGAAAAAGGAACGGAAGTATACAAAAAAGAAACAGATGTAGATGAA 8156

γo ₽ Ş 8217 424 gaggctgctgttcaagcaaagatttagaaaaagcagaacaatactatcacaaaattcct 483 GAAGACGACGAAGAAACAAAAGTAGAAGAAAAGAAAAACAGAAAA-----AAGACGAA gcaacttacatcgatgcttacaactatgcaacaaaattagacgaaatgcgccaagagcta 423 8267

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Ϋ́ 밁 8268 484 GAGGGAACAGATTATGAAGAAGATACAGATGATTCAGACAAAGATGAAGAAACAAAAGTA 832

밁 tatgaaattaaaactcgcacagtcattttagatcgcgtatatggtaaaacaactcgtgat 543 GAAGAAAAGAAAACAGAAAGAGACGAAGAAGAACTGAAGAAGACGAAAAAGAAACAGAA 8387

δô 많 8388 5 ttacttcgctctacatttagagcaaaagcacaagaacttcgcgacagcttaatttatgat 603 GTAGAAAAAAAGAAAACAGAAAAAAGACGAAGAGGGAACAGATTATGAAGAAGATACAGAT 8447

Qy 밁 8448 GATTCAGACAAAGATGTAGAAACAGAAGTAGAAGAACAGACGCAGAAGACAAAGAAGAA 8507

8 γ aaagctaaagctgctgttgatcaaatcaatcaatacttaccaaaagtaacagatgctttc 723 AACGAAGAGGGAACAGATGATGAAGAAGACAAAGTAGAAGAACAGACCTAGACGACCAA 8567

> 밁 8568 GAAGAAGACGGAGAAGAAGATAAAGAAGACGACAAAGAAAAAAGACAAAG 8616

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